

0280

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/023,219

DATE: 01/11/2002

TIME: 12:38:58

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3 <110> APPLICANT: Myriad Genetics, Inc.
4     Cimborra, Daniel M.
5     Heichman, Karen
6     Bartel, Paul L.
8 <120> TITLE OF INVENTION: Protein-Protein Interactions
10 <130> FILE REFERENCE: 2318-282-II
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/023,219
C--> 12 <141> CURRENT FILING DATE: 2001-12-20
12 <150> PRIOR APPLICATION NUMBER: US 60/256,983
13 <151> PRIOR FILING DATE: 2000-12-21
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 40
21 <212> TYPE: DNA
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24 <220> FEATURE:
25 <223> OTHER INFORMATION: oligonucleotide primer
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32 <211> LENGTH: 39
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C--> 34 <213> ORGANISM: Artificial
36 <220> FEATURE:
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39 <400> SEQUENCE: 2
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44 <211> LENGTH: 10625
45 <212> TYPE: DNA
46 <213> ORGANISM: Homo sapiens
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (544)..(6960)
52 <400> SEQUENCE: 3
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55 agccagagcc tgcagcacct tagtaacaga aaaactgata attaggagaa gagacctgtc          120
57 caagaccagg aacctggacc aaaattgtgc catgttgctt tactttaatg agtggcccca          180
59 gtaaaaactg agctgtatgg cagagctgtt cacatttata ttctgtgtcc acccagttct          240
61 gctgaaaccc ctggcaagat cgtggccctg ttgtagcttg tcatgttttg aacagctgtc          300
63 tatggaaaga aagcaaacac aacctagagc aacattgatt tgttttagaa agctctttta          360
65 ttttcagttc tggctgtgtt caacatctta gcttacgttt ttcattgttg aatgatctgc          420
67 cgtatggacg atcacctcta agttagagag ttctgttaatt tggcttgat taaagatgct          480
69 tggttagtga aagctgctgc tttttttata gtcaaaggac tggttctgag agccttggtg          540
71 cag atg gct gag gtc acc gtc cca agg gtg tat gtc gtg ttt ggc atc          588
72 Met Ala Glu Val Thr Val Pro Arg Val Tyr Val Val Phe Gly Ile

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75	cat tgc atc atg gcg aag gca tct tca gat gtg cag gtt tca ggc ttt	636			
76	His Cys Ile Met Ala Lys Ala Ser Ser Asp Val Gln Val Ser Gly Phe				
77		20	25	30	
79	cat cgg aaa atc cag cac gtt aaa aat gaa ctt tgc cac atg ttg agc	684			
80	His Arg Lys Ile Gln His Val Lys Asn Glu Leu Cys His Met Leu Ser				
81		35	40	45	
83	ttg gag gag gtg gcc cca gtg ctg cag cag aca tta ctt cag gac aac	732			
84	Leu Glu Glu Val Ala Pro Val Leu Gln Gln Thr Leu Leu Gln Asp Asn				
85		50	55	60	
87	ctc ttg ggc agg gta cat ttt gac caa ttt aaa gaa gca tta ata ctc	780			
88	Leu Leu Gly Arg Val His Phe Asp Gln Phe Lys Glu Ala Leu Ile Leu				
89		65	70	75	
91	atc ttg tcc aga act ctg tca aat gaa gaa cac ttt caa gaa cca gac	828			
92	Ile Leu Ser Arg Thr Leu Ser Asn Glu Glu His Phe Gln Glu Pro Asp				
93	80	85	90	95	
95	tgc tca cta gaa gct cag ccc aaa tat gtt aga ggt ggg aag cgt tac	876			
96	Cys Ser Leu Glu Ala Gln Pro Lys Tyr Val Arg Gly Gly Lys Arg Tyr				
97		100	105	110	
99	gga cga agg tcc ttg ccc gag ttc caa gag tcc gtg gag gag ttt cct	924			
100	Gly Arg Arg Ser Leu Pro Glu Phe Gln Glu Ser Val Glu Glu Phe Pro				
101		115	120	125	
103	gaa gtg acg gtg att gag cca ctg gat gaa gaa gcg cgg cct tca cac	972			
104	Glu Val Thr Val Ile Glu Pro Leu Asp Glu Glu Ala Arg Pro Ser His				
105		130	135	140	
107	atc cca gcc ggt gac tgc agt gag cac tgg aag acg caa cgc agt gag	1020			
108	Ile Pro Ala Gly Asp Cys Ser Glu His Trp Lys Thr Gln Arg Ser Glu				
109		145	150	155	
111	gag tat gaa gcg gaa ggc cag tta agg ttt tgg aac cca gat gac ttg	1068			
112	Glu Tyr Glu Ala Glu Gly Gln Leu Arg Phe Trp Asn Pro Asp Asp Leu				
113	160	165	170	175	
115	aat gct tca cag agt gga tct tcc cct ccc caa gac tgg ata gaa gag	1116			
116	Asn Ala Ser Gln Ser Gly Ser Ser Pro Pro Gln Asp Trp Ile Glu Glu				
117		180	185	190	
119	aaa ctg caa gaa gtt tgt gaa gat ttg ggg atc acc cgt gat ggt cac	1164			
120	Lys Leu Gln Glu Val Cys Glu Asp Leu Gly Ile Thr Arg Asp Gly His				
121		195	200	205	
123	ctg aac cgg aag aag ctg gtc tcc atc tgt gag cag tat ggt tta cag	1212			
124	Leu Asn Arg Lys Lys Leu Val Ser Ile Cys Glu Gln Tyr Gly Leu Gln				
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127	aat gtg gat gga gag atg ctc gag gaa gta ttc cat aat ctt gat cct	1260			
128	Asn Val Asp Gly Glu Met Leu Glu Glu Val Phe His Asn Leu Asp Pro				
129		225	230	235	
131	gac ggt aca atg agt gta gaa gat ttt ttc tat ggt ttg ttt aaa aat	1308			
132	Asp Gly Thr Met Ser Val Glu Asp Phe Phe Tyr Gly Leu Phe Lys Asn				
133	240	245	250	255	
135	gga aaa tct ctt aca cca tca gca tct act cca tat aga caa cta aaa	1356			
136	Gly Lys Ser Leu Thr Pro Ser Ala Ser Thr Pro Tyr Arg Gln Leu Lys				
137		260	265	270	

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141				275					280					285			
143	acc	tca	tca	gca	atg	aca	agt	acc	att	ggc	ttt	cgg	gtc	ttc	tcc	tgc	1452
144	Thr	Ser	Ser	Ala	Met	Thr	Ser	Thr	Ile	Gly	Phe	Arg	Val	Phe	Ser	Cys	
145			290					295					300				
147	ctg	gat	gat	ggg	atg	ggc	cat	gca	tct	gtg	gag	aga	ata	ctg	gac	acc	1500
148	Leu	Asp	Asp	Gly	Met	Gly	His	Ala	Ser	Val	Glu	Arg	Ile	Leu	Asp	Thr	
149		305					310					315					
151	tgg	cag	gaa	gag	ggc	att	gag	aac	agc	cag	gag	atc	ctg	aag	gcc	ttg	1548
152	Trp	Gln	Glu	Glu	Gly	Ile	Glu	Asn	Ser	Gln	Glu	Ile	Leu	Lys	Ala	Leu	
153	320					325				330					335		
155	gat	ttc	agc	ctc	gat	gga	aac	atc	aat	ttg	aca	gaa	tta	aca	ctg	gcc	1596
156	Asp	Phe	Ser	Leu	Asp	Gly	Asn	Ile	Asn	Leu	Thr	Glu	Leu	Thr	Leu	Ala	
157				340					345					350			
159	ctt	gaa	aat	gaa	ctt	ttg	gtt	acc	aag	aac	agc	att	cac	cag	gcg	gct	1644
160	Leu	Glu	Asn	Glu	Leu	Leu	Val	Thr	Lys	Asn	Ser	Ile	His	Gln	Ala	Ala	
161			355					360					365				
163	ctg	gcc	agc	ttt	aag	gct	gaa	atc	cgg	cat	ttg	ttg	gaa	cga	gtt	gat	1692
164	Leu	Ala	Ser	Phe	Lys	Ala	Glu	Ile	Arg	His	Leu	Leu	Glu	Arg	Val	Asp	
165		370					375					380					
167	cag	gtg	gtc	aga	gaa	aaa	gag	aag	cta	cgg	tca	gat	ctg	gac	aag	gcc	1740
168	Gln	Val	Val	Arg	Glu	Lys	Glu	Lys	Leu	Arg	Ser	Asp	Leu	Asp	Lys	Ala	
169		385				390				395							
171	gag	aag	ctc	aag	tct	tta	atg	gcc	tcg	gag	gtg	gat	gat	cac	cat	gcg	1788
172	Glu	Lys	Leu	Lys	Ser	Leu	Met	Ala	Ser	Glu	Val	Asp	Asp	His	His	Ala	
173	400				405				410					415			
175	gcc	ata	gag	cgg	cgg	aat	gag	tac	aac	ctc	agg	aaa	ctg	gat	gga	gag	1836
176	Ala	Ile	Glu	Arg	Arg	Asn	Glu	Tyr	Asn	Leu	Arg	Lys	Leu	Asp	Gly	Glu	
177				420				425					430				
179	tac	aag	gag	cga	ata	gca	gcc	tta	aaa	aat	gaa	ctc	cga	aaa	gag	aga	1884
180	Tyr	Lys	Glu	Arg	Ile	Ala	Ala	Leu	Lys	Asn	Glu	Leu	Arg	Lys	Glu	Arg	
181			435				440				445						
183	gag	cag	atc	ctg	cag	cag	gca	ggc	aag	cag	cgt	tta	gaa	ctt	gaa	cag	1932
184	Glu	Gln	Ile	Leu	Gln	Gln	Ala	Gly	Lys	Gln	Arg	Leu	Glu	Leu	Glu	Gln	
185		450					455				460						
187	gaa	att	gaa	aag	gca	aaa	aca	gaa	gag	aac	tat	atc	cgg	gac	cgc	ctt	1980
188	Glu	Ile	Glu	Lys	Ala	Lys	Thr	Glu	Glu	Asn	Tyr	Ile	Arg	Asp	Arg	Leu	
189		465				470				475							
191	gcc	ctc	tct	tta	aag	gaa	aac	agt	cgt	ctg	gaa	aat	gag	ctt	cta	gaa	2028
192	Ala	Leu	Ser	Leu	Lys	Glu	Asn	Ser	Arg	Leu	Glu	Asn	Glu	Leu	Leu	Glu	
193	480				485				490					495			
195	aat	gca	gag	aag	ttg	gca	gaa	tat	gag	aat	ctg	aca	aac	aaa	ctt	cag	2076
196	Asn	Ala	Glu	Lys	Leu	Ala	Glu	Tyr	Glu	Asn	Leu	Thr	Asn	Lys	Leu	Gln	
197			500				505				510						
199	aga	aat	ttg	gaa	aat	gtg	tta	gca	gaa	aag	ttt	ggt	gac	ctc	gat	cct	2124
200	Arg	Asn	Leu	Glu	Asn	Val	Leu	Ala	Glu	Lys	Phe	Gly	Asp	Leu	Asp	Pro	
201			515				520				525						
203	agc	agt	gct	gag	ttc	ttc	ctg	caa	gaa	gag	aga	ctg	aca	cag	atg	aga	2172

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208	Asn	Glu	Tyr	Glu	Arg	Gln	Cys	Arg	Val	Leu	Gln	Asp	Gln	Val	Asp	Glu	
209		545					550					555					
211	ctc	cag	tct	gag	ctg	gaa	gaa	tat	cgt	gca	caa	ggc	aga	gtg	ctc	agg	2268
212	Leu	Gln	Ser	Glu	Leu	Glu	Glu	Tyr	Arg	Ala	Gln	Gly	Arg	Val	Leu	Arg	
213	560					565					570					575	
215	ctt	ccg	ttg	aag	aac	tca	ccg	tca	gaa	gaa	gtt	gag	gct	aac	agc	ggt	2316
216	Leu	Pro	Leu	Lys	Asn	Ser	Pro	Ser	Glu	Glu	Val	Glu	Ala	Asn	Ser	Gly	
217				580						585				590			
219	ggc	att	gag	ccc	gaa	cac	ggg	ctc	ggt	tct	gaa	gaa	tgc	aat	cca	ttg	2364
220	Gly	Ile	Glu	Pro	Glu	His	Gly	Leu	Gly	Ser	Glu	Glu	Cys	Asn	Pro	Leu	
221			595					600					605				
223	aat	atg	agc	att	gag	gca	gag	ctg	gtc	att	gaa	cag	atg	aaa	gaa	caa	2412
224	Asn	Met	Ser	Ile	Glu	Ala	Glu	Leu	Val	Ile	Glu	Gln	Met	Lys	Glu	Gln	
225		610					615					620					
227	cat	cac	agg	gac	ata	tgt	tgc	ctc	aga	ctg	gag	ctc	gaa	gat	aaa	gtg	2460
228	His	His	Arg	Asp	Ile	Cys	Cys	Leu	Arg	Leu	Glu	Leu	Glu	Asp	Lys	Val	
229		625				630						635					
231	cgc	cat	tat	gaa	aag	cag	ctg	gac	gaa	acc	gtg	gtc	agc	tgc	aag	aag	2508
232	Arg	His	Tyr	Glu	Lys	Gln	Leu	Asp	Glu	Thr	Val	Val	Ser	Cys	Lys	Lys	
233	640					645					650					655	
235	gca	cag	gag	aac	atg	aag	caa	agg	cat	gag	aac	gaa	acg	cgc	acc	tta	2556
236	Ala	Gln	Glu	Asn	Met	Lys	Gln	Arg	His	Glu	Asn	Glu	Thr	Arg	Thr	Leu	
237			660					665					670				
239	gaa	aaa	caa	ata	agt	gac	ctt	aaa	aat	gaa	att	gct	gaa	ctt	cag	ggg	2604
240	Glu	Lys	Gln	Ile	Ser	Asp	Leu	Lys	Asn	Glu	Ile	Ala	Glu	Leu	Gln	Gly	
241			675					680					685				
243	caa	gca	gca	gtg	ctc	aag	gag	gca	cat	cat	gag	gcc	act	tgc	agg	cat	2652
244	Gln	Ala	Ala	Val	Leu	Lys	Glu	Ala	His	His	Glu	Ala	Thr	Cys	Arg	His	
245		690					695					700					
247	gag	gag	gag	aaa	aaa	caa	ctg	caa	gtg	aag	ctt	gag	gag	gaa	aag	act	2700
248	Glu	Glu	Glu	Lys	Lys	Gln	Leu	Gln	Val	Lys	Leu	Glu	Glu	Glu	Lys	Thr	
249		705					710					715					
251	cac	ctg	cag	gag	aag	ctg	agg	ctg	caa	cat	gag	atg	gag	ctc	aag	gct	2748
252	His	Leu	Gln	Glu	Lys	Leu	Arg	Leu	Gln	His	Glu	Met	Glu	Leu	Lys	Ala	
253	720					725					730					735	
255	aga	ctg	aca	cag	gct	caa	gca	agc	ttt	gag	cgg	gag	agg	gaa	ggc	ctt	2796
256	Arg	Leu	Thr	Gln	Ala	Gln	Ala	Ser	Phe	Glu	Arg	Glu	Arg	Glu	Gly	Leu	
257			740							745				750			
259	cag	agt	agc	gcc	tgg	aca	gaa	gag	aag	gtg	aga	ggc	ttg	act	cag	gaa	2844
260	Gln	Ser	Ser	Ala	Trp	Thr	Glu	Glu	Lys	Val	Arg	Gly	Leu	Thr	Gln	Glu	
261			755					760					765				
263	cta	gag	cag	ttt	cac	cag	gag	cag	ctg	aca	agc	ctg	gtg	gag	aaa	cac	2892
264	Leu	Glu	Gln	Phe	His	Gln	Glu	Gln	Leu	Thr	Ser	Leu	Val	Glu	Lys	His	
265		770					775						780				
267	act	ctt	gag	aaa	gag	gag	tta	aga	aaa	gag	ctc	ttg	gaa	aag	cac	caa	2940
268	Thr	Leu	Glu	Lys	Glu	Glu	Leu	Arg	Lys	Glu	Leu	Leu	Glu	Lys	His	Gln	

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269	785	790	795	
271	agg gag ctt cag gag gga agg gaa aaa atg gaa aca gag tgt aat aga	2988		
272	Arg Glu Leu Gln Glu Gly Arg Glu Lys Met Glu Thr Glu Cys Asn Arg			
273	800	805	810	815
275	aga acc tct caa ata gaa gcc cag ttt cag tct gat tgt cag aaa gtc	3036		
276	Arg Thr Ser Gln Ile Glu Ala Gln Phe Gln Ser Asp Cys Gln Lys Val			
277		820	825	830
279	act gag agg tgt gaa agc gct ctg caa agc ctg gag ggg cgc tac cgc	3084		
280	Thr Glu Arg Cys Glu Ser Ala Leu Gln Ser Leu Glu Gly Arg Tyr Arg			
281		835	840	845
283	caa gag ctg aag gac ctc cag gaa cag cag cgt gag gag aaa tcc cag	3132		
284	Gln Glu Leu Lys Asp Leu Gln Glu Gln Gln Arg Glu Glu Lys Ser Gln			
285		850	855	860
287	tgg gaa ttt gag aag gac gag ctc acc cag gag tgt gcg gaa gcc cag	3180		
288	Trp Glu Phe Glu Lys Asp Glu Leu Thr Gln Glu Cys Ala Glu Ala Gln			
289		865	870	875
291	gag ctg ctg aaa gag act ctt aag aga gag aaa aca act tct ctg gtc	3228		
292	Glu Leu Leu Lys Glu Thr Leu Lys Arg Glu Lys Thr Thr Ser Leu Val			
293	880	885	890	895
295	ctg acc cag gag aga gag atg ctg gag aaa aca tac aaa gaa cat ttg	3276		
296	Leu Thr Gln Glu Arg Glu Met Leu Glu Lys Thr Tyr Lys Glu His Leu			
297		900	905	910
299	aac agc atg gtc gtc gag aga cag cag cta ctc caa gac ctg gaa gac	3324		
300	Asn Ser Met Val Val Glu Arg Gln Gln Leu Leu Gln Asp Leu Glu Asp			
301		915	920	925
303	cta aga aat gta tct gaa acc cag caa agc ctg ctg tct gac cag ata	3372		
304	Leu Arg Asn Val Ser Glu Thr Gln Gln Ser Leu Leu Ser Asp Gln Ile			
305		930	935	940
307	ctt gag ctg aag agc agt cac aaa agg gaa ctg agg gag cgt gag gag	3420		
308	Leu Glu Leu Lys Ser Ser His Lys Arg Glu Leu Arg Glu Arg Glu Glu			
309		945	950	955
311	gtc ctg tgc cag gca ggg gct tcg gag cag ctg gcc agc cag cgg ctg	3468		
312	Val Leu Cys Gln Ala Gly Ala Ser Glu Gln Leu Ala Ser Gln Arg Leu			
313	960	965	970	975
315	gaa aga cta gaa atg gaa cat gac cag gaa agg cag gaa atg atg tcc	3516		
316	Glu Arg Leu Glu Met Glu His Asp Gln Glu Arg Gln Glu Met Met Ser			
317		980	985	990
319	aag ctt cta gcc atg gag aac att cac aaa gcg acc tgt gag aca gca	3564		
320	Lys Leu Leu Ala Met Glu Asn Ile His Lys Ala Thr Cys Glu Thr Ala			
321		995	1000	1005
323	gat cga gaa aga gcc gag atg agc aca gaa atc tcc aga ctt cag	3609		
324	Asp Arg Glu Arg Ala Glu Met Ser Thr Glu Ile Ser Arg Leu Gln			
325		1010	1015	1020
327	agt aaa ata aag gaa atg cag cag gca aca tct cct ctc tca atg	3654		
328	Ser Lys Ile Lys Glu Met Gln Gln Ala Thr Ser Pro Leu Ser Met			
329		1025	1030	1035
331	ctt cag agt ggt tgc cag gtg ata gga gag gag gag gtg gaa gga	3699		
332	Leu Gln Ser Gly Cys Gln Val Ile Gly Glu Glu Glu Val Glu Gly			
333		1040	1045	1050

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
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